ATCAGCGCTG GCGCGGCTGC GGCCGCTGCT GCCTACGCGC CATGGAGCAT 50
CGCATCGTGG GCCCCGGCC GTACCGAGCT ACCAGGCTGT GGAATGAGAC 100
CGTGGAGCTT TTTCGTGCTA AGATGCCGTT ACGGAAACAT CGCTGTCGTT 150
TCAAGAGCTA TGAGCATTGT TTCACAGCGG CCGAAGCTGT GGATTGGCTG 200
CATGAGCTGC TGAGGTGCAG TCAAAACTTC GGCCCTGAAG TGACCCGCAA 250
ACAAACGGTC CAGCTGCTAA AAAAATTCCT GAAGAATCAC GTTATTGAAG 300
ACATCAAGGG AAAATGGGGT GAGGAAGATT TTGAAGACAA TCGTCACTTA 350
TACAGATTTC CTCCTTCTTC ACCCCTGAAA CCATATCCAA AGAAGCCCCC 400
AAACCAAAAG GATGTTATTA AATTTCCAGA ATGGAATGAT CTCCCACCAG 450
GCACTTCACA AGAGAACATC CCAGTGAGGC CAGTTGTGAT GAATTCTGAG 500
ATGTGGTACA AGCGTCACAG TATTGCAATT GGAGAGGTGC CAGCTTGCCG 550
TCTTGTCCAC CGGAGACAGC TGACAGAGGC CAATGTAGAA GAGATATGGA 600
AGTCTATGAC ATTATCATAC TTACAGAAAA TTCTTGGCCT GGATTCCTTA 650
GAAGAAGTTT TAGACGTCAA AGTTGTCAAT TCGAAGTTCA TCATCCATAA 700
TGTATATAGT GTTAGCAAGC AGGGAGTTGT TATTCTTGAT GACAAGTCAA 750
AAGAACTTCC TCATTGGGTG CTGTCAGCTA TGAAGTGTTT GGCAAATTGG 800
CCCAACTGTT CTGATTTGAA GCAGCCTATG TACTTGGGAT TTGAAAAAGA 850
TGTCTGTAAA ACCATAGCTG ATTACTATGG TCACTTGAAA GAGCCTCTAC 900
TTACATTTCA TCTTTTTGAT GCTTTTGTCA C**TGTACTGGG TTTGTTACAG 950**
AAGGAGAAAG TGGCAGTTGA AGCATTTCAG ATTTGCTGCC TTCTCCTACC 1000
TCCTGAAAAT AGGAGAAAGT TACAGCTATT GATGAGGATG ATGGCAAGGA 1050
TTTGCTTAAA CAAAGAGATG CCACCCCTGT GTGATGGCTT TGGTACCCGA 1100
ACACTGATGG TTCAGACATT TTCCCGTTGC ATCTTGTGTT CCAAGGATGA 1150
AGTGGACTTG GATGAGTTAT TAGCTGCTAA ATTGGTAACG TTTCTGATGG 1200
ACAATTACCA GGAAATTCTG AAAGTCCCTT TGGCCTTGCA GACCTCTATA 1250
GAGGAGCGTG TGGCTCATCT ACGAAGAGTC CAGATAAAAT ACCCAGGAGC 1300
TGATATGGAT ATCACTTTAT CTGCTCCATC ATTTTGCCGT CAAATTAGTC 1350
CAGAGGAATT TGAATATCAA AGATCATATG GCTCTCAGGA ACCTCTGGCA 1400
GCCTTGTTGG AGGAAGTCAT AACAGATGCC AAACTCTCCA ACAAAGAGAA 1450
AAAGAAGAAA CTGAAGCAGT TTCAGAAATC CTATCCTGAA GTCTATCAAG 1500
AACGATTTCC TACACCAGAA AGTGCAGCAC TTCTGTTTCC TGAAAAACCC 1550
AAACCGAAAC CACAGCTGCT AATGTGGGCA CTAAAGAAGC CTTTCCAACC 1600
ATTTCAAAGA ACTAGAAGTT TTCGAATGTA ATAATACTTC CACAGCAACA 1650
GGTGCTAGAG ACCACTGTTG TTGTTTTGAG TGAATGGTGG TTAGGAGAAA 1700
GACTTTGGTG GTGGAAGAAA GAAAAGCATA AAACAAAGAC TACTGAAATA 1750
TAGATAAAGA TTGCCTTAGT TTTTAAAAAT GTTTGGCCAT TAGTATTTTT 1800
ATAAAACTCA ATGCTAGTTT TAAGTGTATA AATTGGTTAA AATTTATGAG 1850
TCAAATATAT AGTGATAATG TTAACATGTT TGTAATTGCT ACAGAATTTA 1900
AGGGTATTTT TATCTCTGTG CTTTCTTTTT CATGGTGTTT ATTAAATAAT 1950
TGTGTATATA CATCCTAGCT ACTGATATCT TTATTATAGC CTTAAGACTT 2000
AATTTTAAGT CTTAAAAATA GCGTGTATAC TTGAATAAGA AAGACACTGG 2050
GTACTGTTAC TGTGATGCTA TTGACTTAGT AGCCAATTAT CATTTCTCCT 2100
GTATAAATTC CAGTTTTTAT TGCTGCACAT AAATTTTTTA ATGTCTTATA 2150
TTGTGATAGC TATGTCTTTT ATTGCAGATT TATTGGATGT TATGACAGAT 2200
TTTACTAAAG CTAGTGTTTT TATAACATAT ATATTAGTTG ATGTTTACCT 2250

FIG. 1

```
ATAAGTGGAG TAGATTTTCA TCTGCCTGCA ATGGTATAAT TTCAGTCTTA 2300
GCTAAAAATG GAAAGTTGAA CTGGATAAAT TCTTTGGGTA CCCTTAGACC 2350
TCTGATTCTA AGTCAAATGC AAATGGGTTA AATAAAATGA GACTACTTCC 2400
TTTATAAATA TATTTTCATC CTTTTGAAAG TAAGTGAAAT GTAAATAAAC 2450
TTATTTTTTT TAAAAATG                                    2468
```

FIG. 1 CONT.

```
42  ATG GAG CAT CGC ATC GTG GGG CCC GGG CCG TAC CGA GCT ACC AGG
    M   E   H   R   I   V   G   P   G   P   Y   R   A   T   R

87  CTG TGG AAT GAG ACC GTG GAG CTT TTT CGT GCT AAG ATG CCG TTA
    L   W   N   E   T   V   E   L   F   R   A   K   M   P   L

132 CGG AAA CAT CGC TGT CGT TTC AAG AGC TAT GAG CAT TGT TTC ACA
    R   K   H   R   C   R   F   K   S   Y   E   H   C   F   T

177 GCG GCC GAA GCT GTG GAT TGG CTG CAT GAG CTG CTG AGG TGC AGT
    A   A   E   A   V   D   W   L   H   E   L   L   R   C   S

222 CAA AAC TTC GGC CCT GAA GTG ACC CGC AAA CAA ACG GTC CAG CTG
    Q   N   F   G   P   E   V   T   R   K   Q   T   V   Q   L

267 CTA AAA AAA TTC CTG AAG AAT CAC GTT ATT GAA GAC ATC AAG GGA
    L   K   K   F   L   K   N   H   V   I   E   D   I   K   G

312 AAA TGG GGT GAG GAA GAT TTT GAA GAC AAT CGT CAC TTA TAC AGA
    K   W   G   E   E   D   F   E   D   N   R   H   L   Y   R

357 TTT CCT CCT TCT TCA CCC CTG AAA CCA TAT CCA AAG AAG CCC CCA
    F   P   P   S   S   P   L   K   P   Y   P   K   K   P   P

402 AAC CAA AAG GAT GTT ATT AAA TTT CCA GAA TGG AAT GAT CTC CCA
    N   Q   K   D   V   I   K   F   P   E   W   N   D   L   P

447 CCA GGC ACT TCA CAA GAG AAC ATC CCA GTG AGG CCA GTT GTG ATG
    P   G   T   S   Q   E   N   I   P   V   R   P   V   V   M

492 AAT TCT GAG ATG TGG TAC AAG CGT CAC AGT ATT GCA ATT GGA GAG
    N   S   E   M   W   Y   K   R   H   S   I   A   I   G   E

537 GTG CCA GCT TGC CGT CTT GTC CAC CGC AGA CAG CTG ACA GAG GCC
    V   P   A   C   R   L   V   H   R   R   Q   L   T   E   A

582 AAT GTA GAA GAG ATA TGG AAG TCT ATG ACA TTA TCA TAC TTA CAG
    N   V   E   E   I   W   K   S   M   T   L   S   Y   L   Q

627 AAA ATT CTT GGC CTG GAT TCC TTA GAA GAA GTT TTA GAC GTC AAA
```

FIG. 2

```
     K   I   L   G   L   D   S   L   E   E   V   L   D   V   K

672  CTT GTC AAT TCG AAG TTC ATC ATC CAT AAT GTA TAT AGT GTT AGC
     L   V   N   S   K   F   I   I   H   N   V   Y   S   V   S

717  AAG CAG GGA GTT GTT ATT CTT GAT GAC AAG TCA AAA GAA CTT CCT
     K   Q   G   V   V   I   L   D   D   K   S   K   E   L   P

762  CAT TGG GTG CTG TCA GCT ATG AAG TGT TTG GCA AAT TGG CCC AAC
     H   W   V   L   S   A   M   K   C   L   A   N   W   P   N

807  TGT TCT GAT TTG AAG CAG CCT ATG TAC TTG GGA TTT GAA AAA GAT
     C   S   D   L   K   Q   P   M   Y   L   G   F   E   K   D

852  GTC TGT AAA ACC ATA GCT GAT TAC TAT GGT CAC TTG AAA GAG CCT
     V   C   K   T   I   A   D   Y   Y   G   H   L   K   E   P

897  CTA CTT ACA TTT CAT CTT TTT GAT GCT TTT GTC AGT GTA CTG GGT
     L   L   T   F   H   L   F   D   A   F   V   S   V   L   G

942  TTG TTA CAG AAG GAG AAA GTG GCA GTT GAA GCA TTT CAG ATT TGC
     L   L   Q   K   E   K   V   A   V   E   A   F   Q   I   C

987  TGC CTT CTC CTA CCT CCT GAA AAT AGG AGA AAG TTA CAG CTA TTG
     C   L   L   L   P   P   E   N   R   R   K   L   Q   L   L

1032 ATG AGG ATG ATG GCA AGG ATT TGC TTA AAC AAA GAG ATG CCA CCC
     M   R   M   M   A   R   I   C   L   N   K   E   M   P   P

1077 CTG TGT GAT GGC TTT GGT ACC CGA ACA CTG ATG GTT CAG ACA TTT
     L   C   D   G   F   G   T   R   T   L   M   V   Q   T   F

1122 TCC CGT TGC ATC TTG TGT TCC AAG GAT GAA GTG GAC TTG GAT GAG
     S   R   C   I   L   C   S   K   D   E   V   D   L   D   E

1167 TTA TTA GCT GCT AAA TTG GTA ACG TTT CTG ATG GAC AAT TAC CAG
     L   L   A   A   K   L   V   T   F   L   M   D   N   Y   Q

1212 GAA ATT CTG AAA GTC CCT TTG GCC TTG CAG ACC TCT ATA GAG GAG
     E   I   L   K   V   P   L   A   L   Q   T   S   I   E   E

1257 CGT GTG GCT CAT CTA CGA AGA GTC CAG ATA AAA TAC CCA GGA GCT
     R   V   A   H   L   R   R   V   Q   I   K   Y   P   G   A

1302 GAT ATG GAT ATC ACT TTA TCT GCT CCA TCA TTT TGC CGT CAA ATT
     D   M   D   I   T   L   S   A   P   S   F   C   R   Q   I
```

FIG. 2 CONT.-A

```
1347 AGT CCA GAG GAA TTT GAA TAT CAA AGA TCA TAT GGC TCT CAG GAA
      S   P   E   E   F   E   Y   Q   R   S   Y   G   S   Q   E

1392 CCT CTG GCA GCC TTG TTG GAG GAA GTC ATA ACA GAT GCC AAA CTC
      P   L   A   A   L   L   E   E   V   I   T   D   A   K   L

1437 TCC AAC AAA GAG AAA AAG AAG AAA CTG AAG CAG TTT CAG AAA TCC
      S   N   K   E   K   K   K   K   L   K   Q   F   Q   K   S

1482 TAT CCT GAA GTC TAT CAA GAA CGA TTT CCT ACA CCA GAA AGT GCA
      Y   P   E   V   Y   Q   E   R   F   P   T   P   E   S   A

1527 GCA CTT CTG TTT CCT GAA AAA CCC AAA CCG AAA CCA CAG CTG CTA
      A   L   L   F   P   E   K   P   K   P   K   P   Q   L   L

1572 ATG TGG GCA CTA AAG AAG CCT TTC CAA CCA TTT CAA AGA ACT AGA
      M   W   A   L   K   K   P   F   Q   P   F   Q   R   T   R

1617 AGT TTT CGA ATG TAA
      S   F   R   M   *
```

FIG. 2 CONT.-B

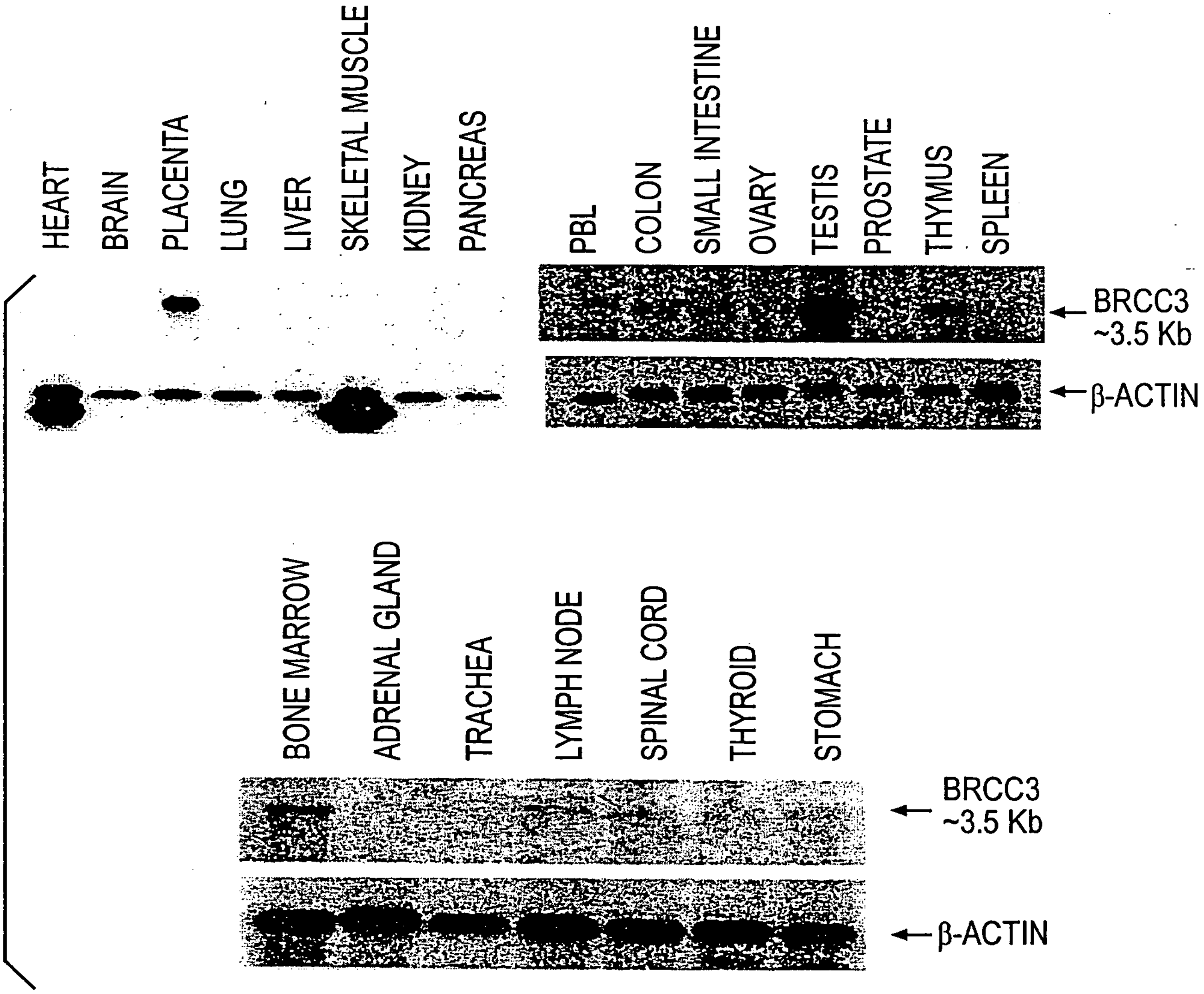
HEART
BRAIN
PLACENTA
LUNG
LIVER
SKELETAL MUSCLE
KIDNEY
PANCREAS
PBL
COLON
SMALL INTESTINE
OVARY
TESTIS
PROSTATE
THYMUS
SPLEEN
BRCC3 ~3.5 Kb
β-ACTIN
BONE MARROW
ADRENAL GLAND
TRACHEA
LYMPH NODE
SPINAL CORD
THYROID
STOMACH
BRCC3 ~3.5 Kb
β-ACTIN

FIG. 3

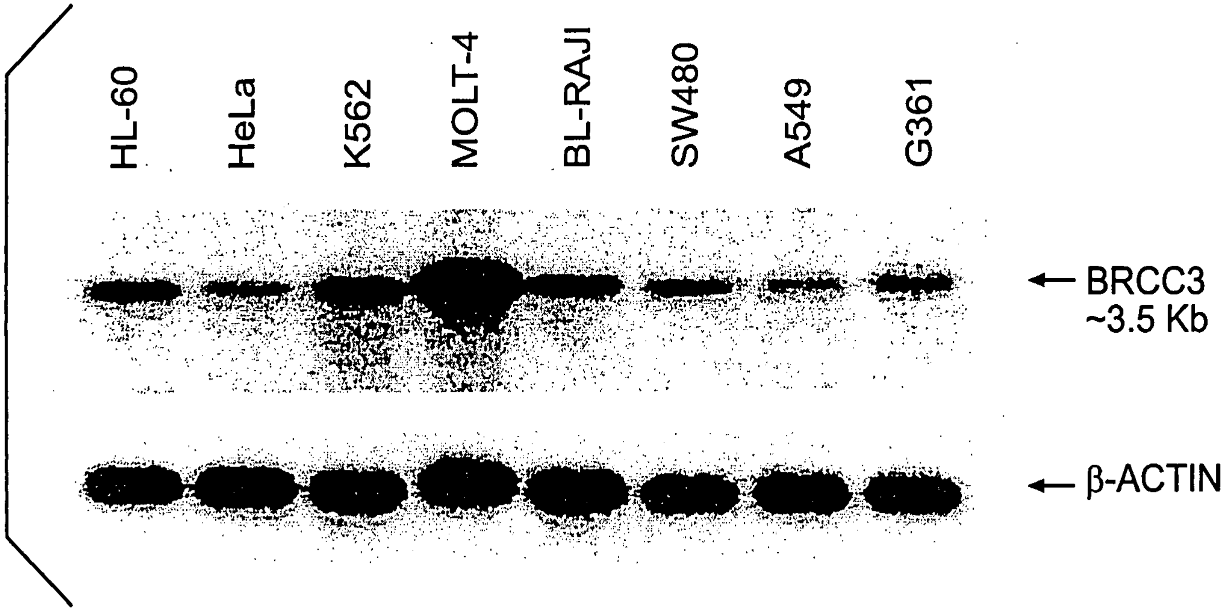
HL-60
HeLa
K562
MOLT-4
BL-RAJI
SW480
A549
G361
BRCC3
~3.5 Kb
β-ACTIN

FIG. 4

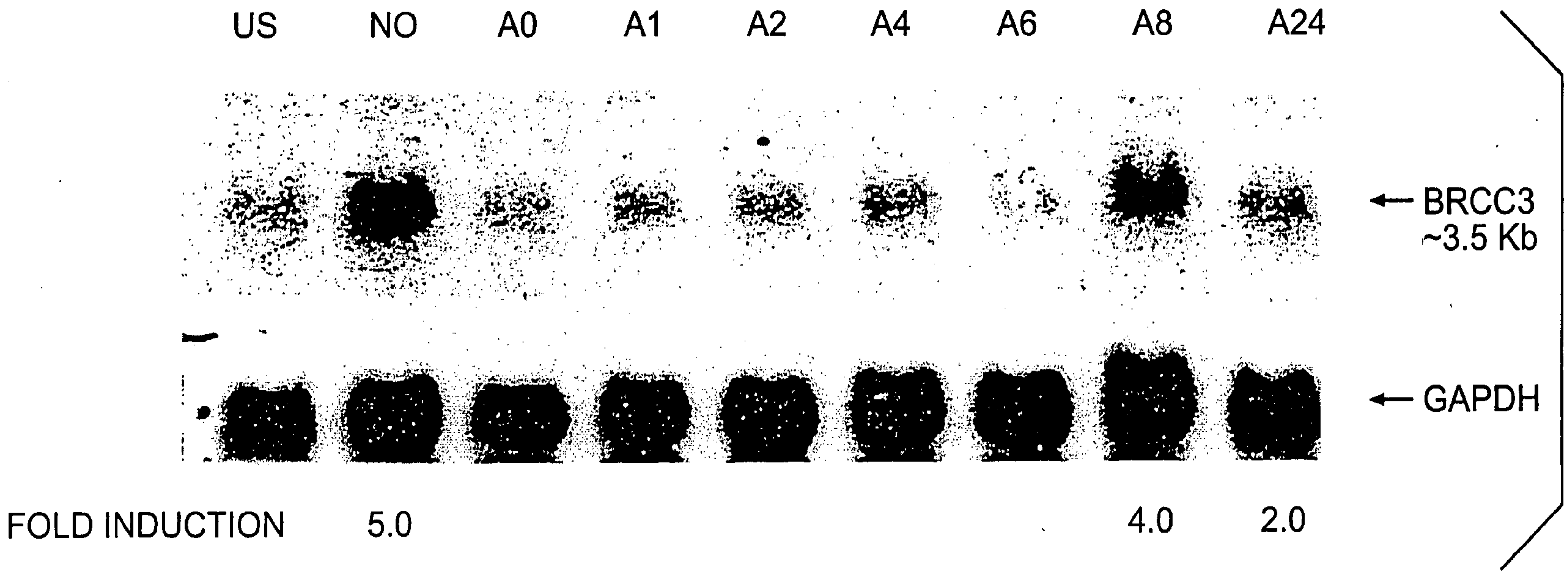
US
NO
A0
A1
A2
A4
A6
A8
A24
← BRCC3 ~3.5 Kb
← GAPDH
FOLD INDUCTION
5.0
4.0
2.0

FIG. 5

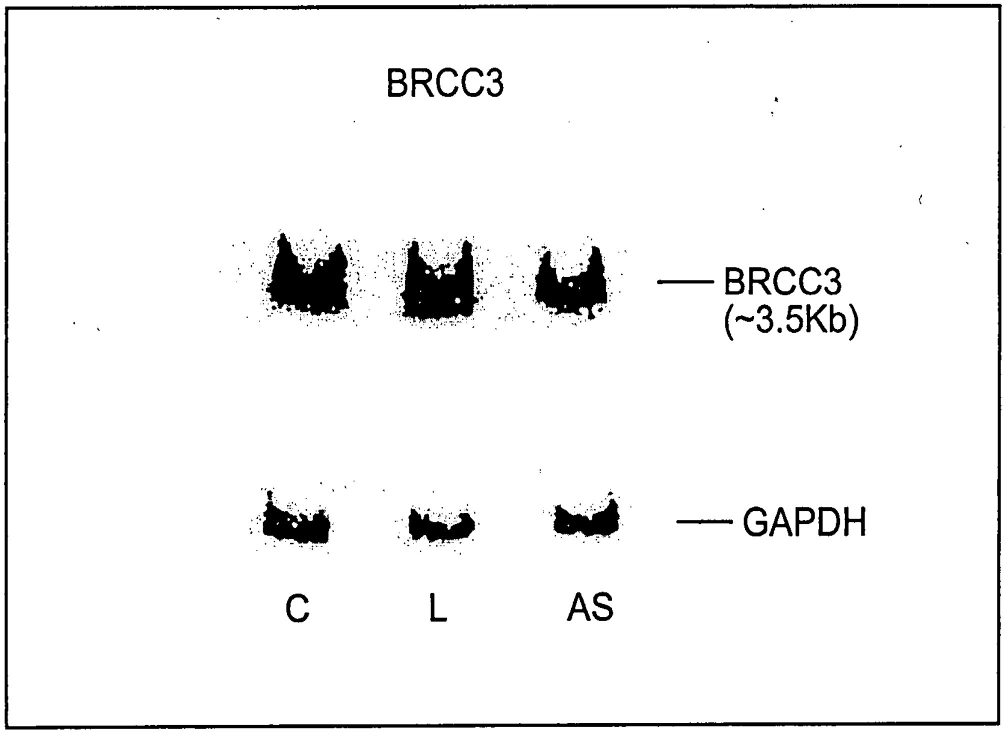

FIG. 6